

SEQUENCE LISTING

<110> Willson, Tracy
 Nicola, Nicos A.
 Hilton, Douglas J.
 Metcalf, Donald
 Zhang, Jian G.

<120> NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
 ENCODING SAME

<130> Davies cc

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 <141> 1998-06-29

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<170> PatentIn Ver. 2.0

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Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp	
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acc gcc acc gtg nnn ggc caa gtt gcc gcg gcc aca gaa gtt cag cca	156
Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro	
20 25 30	
cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata	204
Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile	
35 40 45	
tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga	252
Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg	
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Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu	
65 70 75 80	
act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag	348
Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln	
85 90 95	
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Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu	
100 105 110	
gtg aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg	444
Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val	
115 120 125	
act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc	492
Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser	

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tat Tyr	tgg Trp	tac Tyr	agc Ser 165	agc Ser	ctg Leu	gag Glu	aaa Lys	agt Ser	cgt Arg 170	caa Gln	tgt Cys	gaa Glu	aac Asn	atc Ile 175	tat Tyr	588
aga Arg	gaa Glu	ggt Gly	caa Gln 180	cac His	att Ile	gct Ala	tgt Cys	tcc Ser 185	ttt Phe	aaa Lys	ttg Leu	act Thr	aaa Lys 190	gtg Val	gaa Glu	636
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gct Ala	ggg Gly 210	aaa Lys	att Ile	agg Arg	cca Pro	tcc Ser 215	tgc Cys	aaa Lys	ata Ile	gtg Val	tct Ser 220	tta Leu	act Thr	tcc Ser	tat Tyr	732
gtg Val 225	aaa Lys	cct Pro	gat Asp	cct Pro	cca Pro 230	cat His	att Ile	aaa Lys	cat His	ctt Leu 235	ctc Leu	ctc Leu	aaa Lys	aat Asn	ggt Gly 240	780
gcc Ala	tta Leu	tta Leu	gtg Val 245	cag Gln	tgg Trp	aag Lys	aat Asn	cca Pro	caa Gln 250	aat Asn	ttt Phe	aga Arg	agc Ser 255	aga Arg	tgc Cys	828
tta Leu	act Thr	tat Tyr	gaa Glu 260	gtg Val	gag Glu	gtc Val	aat Asn	aat Asn 265	act Thr	caa Gln	acc Thr	gac Asp	cga Arg 270	cat His	aat Asn	876
att Ile	tta Leu	gag Glu 275	gtt Val	gaa Glu	gag Glu	gac Asp	aaa Lys 280	tgc Cys	cag Gln	aat Asn	tcc Ser 285	gaa Glu	tct Ser	gat Asp	aga Arg	924
aac Asn	atg Met 290	gag Glu	ggt Gly	aca Thr	agt Ser	tgt Cys 295	ttc Phe	caa Gln	ctc Leu	cct Pro	ggt Gly 300	gtt Val	ctt Leu	gcc Ala	gac Asp	972
gct Ala 305	gtc Val	tac Tyr	aca Thr	gtc Val	aga Arg 310	gta Val	aga Arg	gtc Val	aaa Lys	aca Thr 315	aac Asn	aag Lys	tta Leu	tgc Cys	ttt Phe 320	1020
gat Asp	gac Asp	aac Asn	aaa Lys 325	ctg Leu	tgg Trp	agt Ser	gat Asp	tgg Trp	agt Ser 330	gaa Glu	gca Ala	cag Gln	agt Ser	ata Ile 335	ggt Gly	1068
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gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg 1164
 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
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ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt 1212
 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
 370 375 380

aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag 1260
 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
 385 390 395 400

tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg 1308
 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
 405 410 415

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 35 40 45

Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg

Tyr	Phe	Ser	His	Phe	Asp	Asp	Gln	Gln	Asp	Lys	Lys	Ile	Ala	Pro	Glu
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Thr	His	Arg	Lys	Glu	Glu	Leu	Pro	Leu	Asp	Glu	Lys	Ile	Cys	Leu	Gln
				85					90					95	
Val	Gly	Ser	Gln	Cys	Ser	Ala	Asn	Glu	Ser	Glu	Lys	Pro	Ser	Pro	Leu
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Tyr	Trp	Tyr	Ser	Ser	Leu	Glu	Lys	Ser	Arg	Gln	Cys	Glu	Asn	Ile	Tyr
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Pro	Xaa	Ser	Phe	Glu	His	Gln	Asn	Val	Gln	Ile	Met	Val	Lys	Asp	Asn
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Ala	Val	Tyr	Thr	Val	Arg	Val	Arg	Val	Lys	Thr	Asn	Lys	Leu	Cys	Phe
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Asp	Asp	Asn	Lys	Leu	Trp	Ser	Asp	Trp	Ser	Glu	Ala	Gln	Ser	Ile	Gly
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 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
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 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
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Ala	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Pro	Thr	Glu	Thr	Gln	Pro	
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cct	gtg	aca	aat	ttg	agt	gtc	tct	gtt	gaa	aac	ctc	tgc	aca	gta	ata	204
Pro	Val	Thr	Asn	Leu	Ser	Val	Ser	Val	Glu	Asn	Leu	Cys	Thr	Val	Ile	
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Trp	Thr	Trp	Asn	Pro	Pro	Glu	Gly	Ala	Ser	Ser	Asn	Cys	Ser	Leu	Trp	
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Tyr	Phe	Ser	His	Phe	Gly	Asp	Lys	Gln	Asp	Lys	Lys	Ile	Ala	Pro	Glu	

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gtg Val	ggg Gly	tcc Ser	cag Gln 100	tgt Cys	agc Ser	acc Thr	aat Asn	gag Glu 105	agt Ser	gag Glu	aag Lys	cct Pro	agc Ser 110	att Ile	ttg Leu	396
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gtg Val 225	aaa Lys	cct Pro	gat Asp	cct Pro	cca Pro 230	cat His	att Ile	aaa Lys	aac Asn	ctc Leu 235	tcc Ser	ttc Phe	cac His	aat Asn	gat Asp 240	780
gac Asp	cta Leu	tat Tyr	gtg Val	caa Gln 245	tgg Trp	gag Glu	aat Asn	cca Pro	cag Gln 250	aat Asn	ttt Phe	att Ile	agc Ser	aga Arg 255	tgc Cys	828
cta Leu	ttt Phe	tat Tyr	gaa Glu 260	gta Val	gaa Glu	gtc Val	aat Asn 265	aac Asn	agc Ser	caa Gln	act Thr	gag Glu 270	aca Thr	cat His	aat Asn	876
gtt Val	ttc Phe	tac Tyr	gtc Val	caa Gln	gag Glu	gct Ala	aaa Lys	tgt Cys	gag Glu	aat Asn	cca Pro	gaa Glu	ttt Phe	gag Glu	aga Arg	924

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Thr	Leu	Asn	Thr	Val	Arg	Ile	Arg	Val	Lys	Thr	Asn	Lys	Leu	Cys	Tyr	
305					310					315					320	
gag	gat	gac	aaa	ctc	tgg	agt	aat	tgg	agc	caa	gaa	atg	act	ata	gtt	1068
Glu	Asp	Asp	Lys	Leu	Trp	Ser	Asn	Trp	Ser	Gln	Glu	Met	Thr	Ile	Val	
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aag	aag	cgc	aat	tcc	aca	ctc	tac	ata	acc	atg	tta	ctc	att	gtt	cca	1116
Lys	Lys	Arg	Asn	Ser	Thr	Leu	Tyr	Ile	Thr	Met	Leu	Leu	Ile	Val	Pro	
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gtc	atc	gtc	gca	ggg	gca	atc	ata	gta	ctc	ctg	ctt	tac	cta	aaa	agg	1164
Val	Ile	Val	Ala	Gly	Ala	Ile	Ile	Val	Leu	Leu	Leu	Tyr	Leu	Lys	Arg	
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ctc	aag	att	att	ata	ttc	cct	cca	att	cct	gat	cct	ggc	aag	att	ttt	1212
Leu	Lys	Ile	Ile	Ile	Phe	Pro	Pro	Ile	Pro	Asp	Pro	Gly	Lys	Ile	Phe	
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aaa	gaa	atg	ttt	gga	gac	cag	aat	gat	gat	act	ctg	cac	tgg	aag	aag	1260
Lys	Glu	Met	Phe	Gly	Asp	Gln	Asn	Asp	Asp	Thr	Leu	His	Trp	Lys	Lys	
385					390					395					400	
tac	gac	atc	tat	gag	aag	caa	acc	aag	gag	gaa	acc	gac	tct	gta	gtg	1308
Tyr	Asp	Ile	Tyr	Glu	Lys	Gln	Thr	Lys	Glu	Glu	Thr	Asp	Ser	Val	Val	
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ctg	ata	gaa	aac	ctg	aag	aaa	gcc	tct	cag	tgatggagat	aattttatttt					1358
Leu	Ile	Glu	Asn	Leu	Lys	Lys	Ala	Ser	Gln							
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Trp	Thr	Trp	Asn	Pro	Pro	Glu	Gly	Ala	Ser	Ser	Asn	Cys	Ser	Leu	Trp
	50					55					60				
Tyr	Phe	Ser	His	Phe	Gly	Asp	Lys	Gln	Asp	Lys	Lys	Ile	Ala	Pro	Glu
65					70					75					80
Thr	Arg	Arg	Ser	Ile	Glu	Val	Pro	Leu	Asn	Glu	Arg	Ile	Cys	Leu	Gln
				85					90					95	
Val	Gly	Ser	Gln	Cys	Ser	Thr	Asn	Glu	Ser	Glu	Lys	Pro	Ser	Ile	Leu
			100					105					110		
Val	Glu	Lys	Cys	Ile	Ser	Pro	Pro	Glu	Gly	Asp	Pro	Glu	Ser	Ala	Val
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Thr	Glu	Leu	Gln	Cys	Ile	Trp	His	Asn	Leu	Ser	Tyr	Met	Lys	Cys	Ser
130						135					140				
Trp	Leu	Pro	Gly	Arg	Asn	Thr	Ser	Pro	Asp	Thr	Asn	Tyr	Thr	Leu	Tyr
145					150					155					160
Tyr	Trp	His	Arg	Ser	Leu	Glu	Lys	Ile	His	Gln	Cys	Glu	Asn	Ile	Phe
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Arg	Glu	Gly	Gln	Tyr	Phe	Gly	Cys	Ser	Phe	Asp	Leu	Thr	Lys	Val	Lys
			180					185					190		
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Leu	Phe	Tyr	Glu	Val	Glu	Val	Asn	Asn	Ser	Gln	Thr	Glu	Thr	His	Asn
			260					265					270		
Val	Phe	Tyr	Val	Gln	Glu	Ala	Lys	Cys	Glu	Asn	Pro	Glu	Phe	Glu	Arg
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Asn	Val	Glu	Asn	Thr	Ser	Cys	Phe	Met	Val	Pro	Gly	Val	Leu	Pro	Asp
	290					295					300				

Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr
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 Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Thr Ile Val
 325 330 335
 Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro
 340 345 350
 Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg
 355 360 365
 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
 370 375 380
 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
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 <213> N-terminal FLAG epitope-tag

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<213> Oligo 1478 5'

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<212> DNA

<213> Oligo 1480 5'

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